Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk / Erratum

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Editorial Note

Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk

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We the editors of Cell have been informed by the Lead Contact and corresponding author of this paper, Dr. Chris Cotsapas, that further analyses following the publication of the paper have indicated that two variants (rs61999302 encoding PRKRA.D33G and rs62176112 encoding PRKRA.P11L) reported in this paper to be associated with MS risk were in fact spurious associations due to the presence of a dispersed duplication event, in which this region of chromosome 2 is duplicated in the MHC region of chromosome 6. The potential for this dispersed duplication to lead to spurious associations has been previously documented (Wellcome Trust Case Control Consortium et al., 2010). Upon learning of the potential problems associated with signals in this region, the authors used the data reported in this paper to impute classical HLA alleles and amino acid variants using SNP2HLA (Jia et al. 2013) and found that the two reported variants in PRKRA showed extensive linkage disequilibrium with genotyped and imputed HLA variants, including known MS risk alleles. Conditioning on any of these known variants was sufficient to explain the reported association, leading to the conclusion that these two signals are driven by the duplication and are not true associations of the reported variants with MS risk. With this note, we and the authors would like to alert readers to this issue. The remaining findings in the paper are unchanged, as are the main conclusions of the paper. The authors would also like to thank Dr. Matthew Hurles (Wellcome Sanger Institute) for bringing this issue to their attention.

Furthermore, in the printed version of the experimental model and subject details section of the STAR methods, Köln is listed as one of the patient recruitment centers, but Düsseldorf should have been listed instead. One of the authors, Dr. Clemens Warnke, although currently based in Köln, in fact contributed patient samples collected in Düsseldorf to the study. This has been corrected in the article online, and the authors apologize for any confusion these issues may have caused.

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